

|||||
 MTTTVALSNEFAKINEEDLSFEPPLSLVOLMHAQRFLLSSWSGVIPFEFSCSCLPFLYPPKWRQIHDLDKT
 X 10 20 30 40 50 60 70

80
 KRICCYRSGFMSNLIFEFCGADAKKL

OYLNSS
 X

9. US-09-746-783-19 (1-107)

US-09-096-287-2 Sequence 2, Application US/09096287

Initial Score = 13 Optimized Score = 48 Significance = 0.18
 Residue Identity = 11% Matches = 12 Mismatches = 89
 Gaps = 0 Conservative Substitutions = 6

X 10 20 30 40 50 60
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCHIKITPTFOMKRSQVTLF
 MFLSLCIGHTSTSYLPLQPHLPPLTRAHHIIONETAPSSSEHITLONPHLCVTLIRHSAKAPPCCFRALPF
 X 10 20 30 40 50 60 70

70 80 90 100 X
 SRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOELM
 LPFIHPPLCIFIKTLHNLIYLSYHILKNCFFHSLITRM
 80 90 100 110

10. US-09-746-783-19 (1-107)

US-09-185-936-12 Sequence 12, Application US/09185936

Initial Score = 13 Optimized Score = 48 Significance = 0.18
 Residue Identity = 8% Matches = 11 Mismatches = 89
 Gaps = 19 Conservative Substitutions = 7

X 10 20 30 40 50
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCHIK
 FEKANQLAFVILAIICLFAKSLIVSVCLPISAPPELSLEMRHNPITALPSQILPHEAPQOSTSLK
 10 20 X 30 40 50 60 70
 TIPTFQMFK-----KSQKVTLPFSRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOE
 60 70 80 90 100
 FOESNSTYTYTFTIRKRIYVLNRTSPMSQLPVFLACQARHMRPFCLEIYLPULLGLRGHLSLPTMET
 80 90 100 110 120 130 140 150

X
 LM
 KSS
 X

11. US-09-746-783-19 (1-107)

US-09-096-287-4 Sequence 4, Application US/09096287

Initial Score = 13 Optimized Score = 47 Significance = 0.18
 Residue Identity = 7% Matches = 8 Mismatches = 88
 Gaps = 1 Conservative Substitutions = 10

X 10 20 30 40 50
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCHIK
 MDDGRRRRPIAGGGSPKDLIEDIVGGGKPKDGKGDGRYSNDPDSGVAEPETIAGVASALAMALIG
 100 110 X 120 130 140 150 160

60 70 80 90 100 X
 TIPTFQMFKRSQKVTLPFSRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOELM
 : : : : :
 : : : : :
 : : : : :

AVSSYSTYQO-KKFCSTISQGLNADYKGENLEAVCOEPOVRYSTLHTQSAEPPPPBPARI
 170 180 190 200 210 220

12. US-09-746-783-19 (1-107)

US-09-130-189-4 Sequence 4, Application US/09130189

Initial Score = 13 Optimized Score = 48 Significance = 0.18
 Residue Identity = 11% Matches = 13 Mismatches = 88
 Gaps = 2 Conservative Substitutions = 6

X 10 20 30 40 50
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCH--IKTI
 MGSQHSAAARSSCRKROEDDRDGLAEROEFAIAOPPYVEFTGRDSICLNCQGTGYPTEQVNLVALI
 10 X 20 30 40 50 60 70

60 70 80 90 100 X
 PTFOMKRSQKVTLPFSRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOELM
 PHSDQRLRPQRTQOYVLLSTLLCLASGLVVFPLPHSVLAVDDGIVKAVTENVKODSLVITMATKIRN
 80 90 100 110 120 X 130 140

S

13. US-09-746-783-19 (1-107)

US-09-092-722-4 Sequence 4, Application US/09092722

Initial Score = 13 Optimized Score = 48 Significance = 0.18
 Residue Identity = 5% Matches = 6 Mismatches = 96
 Gaps = 0 Conservative Substitutions = 5

X 10 20 30 40 50
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCHIK
 WKLKAVDAFKSAPLYORPGYSAPOPTLPSEFPLEPSAKLSHVTGIDTKDKSLKTVSSGAKKSFELL
 130 140 150 160 170 180 190
 TIPTFOMKRSQKVTLPFSRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOELM
 SESDGLAMHEPVSQVRKRTKVEFNLTDMPETPEINHLKEPPEOSTNHTTLKIDHMDPYMLNREDAHS
 200 210 220 230 240 250 260

14. US-09-746-783-19 (1-107)

US-09-149-633-8 Sequence 8, Application US/09149633

Initial Score = 13 Optimized Score = 51 Significance = 0.18
 Residue Identity = 10% Matches = 11 Mismatches = 92
 Gaps = 0 Conservative Substitutions = 4

X 10 20 30 40 50
 MVOIINKDNEFKTFLTAAGHKLAVVOFSSKRCGPCKRMFPVHELAETCHIK
 TCOVVMQKVSVCIPITSEHLSLKRKAQOEPEYSKRIARPNMAERETESNSKDDKAASSERKGCANAN
 60 70 X 80 90 100 110 120

60 70 80 90 100 X
 TIPTFOMKRSQKVTLPFSRIKRICCYRSGFMSNLIFEFCGADAKKLEAKTOELM
 SPFGSSSTTKGSESTIVSDKNENFCGLADQETGSKNIVSCDSNIGADKYEKKKOTLOHVOGEMELKGCSSENII
 130 140 150 160 170 180 X 190
 LSD
 200

15. US-09-746-783-19 (1-107)

US-09-130-189-6 Sequence 6, Application US/09130189

[illegible]

	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400
GTTCGACGACCTCATGTGMAAACAGAGAAACATCCCTTTTGCAGGGGACACACCGTTTCGAGAAATAATGAAACC	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420
GGAGAGAAACACACA-GTGGCACCGGAGGACACCGACCTGAGCAGGACACTGCGAGGCTGGGACAGAGTACAGAA	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470
ACTGCGAGTTGTGTGCCGACGCTGTGMAAAATGTTTTAAATTCATTCGTGTCTTTAAATATCTGTACCATGT	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490
GCACGGCTGCACAGGACGAGGAGCTGTGACCCAGGGGCTTAGAGCCGGGACAGGAGACTGGTGTGGACCTGGGG	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540
ATTACACCGAGGAAGTGTGTAATAATCCCTGTT-----GTTTAGTTGATTCACCTGTAGCTGTCTCC	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570
AGGAGGACAGAGAGCCTTAAAGCAGCAGCACCGCTGTATTCACGACGAGGAGTGAATCAAGAAAGATGGAAC	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610
TATTTATTACAGTATCC	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630
GCGGCCAGGCCAAT	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680
520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690
X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Initial Score = 69	Optimized Score = 168	Significance = 2.19															
Residue Identity = 37%	Matches = 179	Mismatches = 296															
Gaps = 6	Conservative Substitutions = 0																
3. US-09-746-783-18' (1-481)																	
US-09-098-588-19	Sequence 19,	Application US/09098588															
TCAGACATATTTCTGTGACGTGTTCACAGTATTGGCAGCTCCAAATACGATATGGTTCTATTATACACTGTG	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440
GTATTTTCCCTTGGAGATCAGCTTATATATTCGTGAGCTGTGGCTTCCAAATTTTATAGCATGGGCTCCAC	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220
GGCTTTCATGTGTGGAGTGTGCTCTTACAGCATGCCGATCTACAGATGCTTTTACTGTGCCG	360	370	380	390	400	410	420	430	440	450	460	470	480				

410 420 430 440 450 460
TACACAGGGAAGTCTCATG-----AAATCCCTCTTGGTTAATTGGACACAGTACCTGTCCTATT
- | | | | | - | | | | | - | | | | | - | | | | |
CTATGTTGCCCTTTGAGTATGATGCTCCAGAGGCTTACGACTGCTCTTCAGATGATTAAGAGGACGCTTGCTGTG

TACAGTATCC
 |
 |
 AACCAAAAAAAAAAAAAAAAAA
 1240 1250 1260

x	10	20	30	40	50
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AAAAAA
2480

> 0 <
01 10 IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-746-783-18.res made by bobryen on Tue Jun 18 102 14:35:57-PDT.

Query sequence being compared: US-09-746-783-18 (1-481)
Number of sequences searched: 154
Number of scores above cutoff: 154

Results of the initial comparison of US-09-746-783-18 (1-481) with:
File : US08958304.seq
File : US09092722.seq
File : US09066287.seq
File : US09085888.seq
File : US09130189.seq
File : US09149633.seq
File : US09165960A.seq
File : US09185936.seq

100-
N - *
U 50-
M -
B -
R -
O -
F 10-
S -
E 5- *
Q -
U -
E -
N -
C -
S -
SCORE 0 | 53 | 107 | 160 | 214 | 267 | 321 | 374 | 428 | 481 |
STDEV 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
PARAMETERS
Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 481
Gap size penalty 0.33
Cutoff score 1
Randomization group 0
SEARCH STATISTICS
Scores: Mean Median Standard Deviation
29 23 41.90
Times: CPU
00:00:00.95 Total Elapsed
00:00:01.00

Number of residues: 126429
Number of sequences searched: 154
Number of scores above cutoff: 154
The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Init. Opt. Sig. Frame
1. US-09-092-722-18	Sequence 18, Application	481	481	481 10.79 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt. Sig. Frame
2. US-09-096-287-7	Sequence 7, Application US	568	113	194 2.00 0
3. US-09-149-633-7	Sequence 7, Application US	2487	89	189 1.43 0
4. US-09-098-588-3	Sequence 3, Application US	2298	80	193 1.22 0
5. US-08-958-304-9	Sequence 9, Application US	1325	69	185 0.95 0
6. US-08-958-304-19	Sequence 19, Application	1257	68	185 0.93 0
7. US-09-165-960-13	Sequence 13, Application	1110	65	185 0.86 0
8. US-09-185-936-5	Sequence 5, Application US	1108	64	184 0.84 0
9. US-09-165-960-14	Sequence 14, Application	861	61	168 0.76 0
10. US-09-096-287-9	Sequence 9, Application US	2773	59	179 0.72 0
11. US-09-185-936-9	Sequence 9, Application US	1294	58	172 0.69 0
12. US-09-149-633-15	Sequence 15, Application	984	57	175 0.67 0
13. US-09-096-287-17	Sequence 17, Application	1309	55	158 0.62 0
14. US-08-958-304-17	Sequence 17, Application	1598	54	173 0.60 0
15. US-09-098-588-15	Sequence 15, Application	1240	53	189 0.57 0
16. US-09-185-936-3	Sequence 3, Application US	1276	53	187 0.57 0
17. US-08-958-304-3	Sequence 3, Application US	2859	53	173 0.57 0
18. US-09-096-287-15	Sequence 15, Application	1694	52	170 0.55 0
19. US-09-092-722-5	Sequence 5, Application US	884	51	185 0.53 0
20. US-09-149-633-5	Sequence 5, Application US	2120	51	184 0.53 0
21. US-09-165-960-5	Sequence 5, Application US	1573	50	189 0.50 0
22. US-09-130-189-7	Sequence 7, Application US	1865	50	165 0.50 0
23. US-09-092-722-12	Sequence 12, Application	2343	50	173 0.50 0
24. US-09-098-588-13	Sequence 13, Application	722	48	179 0.45 0
25. US-09-185-936-11	Sequence 11, Application	1354	48	167 0.45 0
26. US-09-149-633-11	Sequence 11, Application	1398	48	168 0.45 0
27. US-09-096-287-13	Sequence 13, Application	1592	47	178 0.43 0
28. US-09-130-189-11	Sequence 11, Application	2069	47	168 0.43 0
29. US-09-096-287-19	Sequence 19, Application	1740	46	175 0.41 0
30. US-09-185-936-1	Sequence 1, Application US	2556	46	157 0.41 0
31. US-08-165-960-11	Sequence 11, Application	883	45	171 0.38 0
32. US-09-130-189-9	Sequence 9, Application US	2094	45	183 0.38 0
33. US-09-149-633-13	Sequence 13, Application	2132	45	172 0.38 0
34. US-09-092-722-9	Sequence 9, Application US	75	43	47 0.33 0
35. US-09-130-189-17	Sequence 17, Application	791	42	185 0.31 0
36. US-09-092-722-3	Sequence 3, Application US	1263	42	177 0.31 0
37. US-09-130-189-3	Sequence 3, Application US	1425	42	180 0.31 0
38. US-09-149-633-9	Sequence 9, Application US	3495	42	186 0.31 0
39. US-08-958-304-5	Sequence 5, Application US	933	41	174 0.29 0
40. US-09-185-936-17	Sequence 17, Application	1056	41	171 0.29 0
41. US-09-165-960-9	Sequence 9, Application US	510	40	171 0.26 0
42. US-09-165-960-3	Sequence 3, Application US	1472	40	173 0.26 0
43. US-09-130-189-1	Sequence 1, Application US	2271	40	169 0.26 0
44. US-09-185-936-7	Sequence 7, Application US	2952	39	156 0.24 0
45. US-08-958-304-12	Sequence 12, Application	533	38	154 0.21 0

1. US-09-746-783-18 (1-481)
US-09-092-722-18 Sequence 18, Application US/09092722

Initial Score = 481 Optimized Score = 481 Significance = 10.79
Residue Identity = 100% Matches = 481 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
GGATCTGTATTAATATGAGACAGCTACAGTCCAGCTAAACCAACAGGAGGATTTTCATCAGCACCTCC
|||||

[illegible]

AGTGGCTCTTCCCTGTTGACATGACCCCGCTTACAGCAAGACACAGCCATGACAAACCCAGATG
610 620 630 640 650 660 670

480
AAAAAA

CATGCTCTTCCCTCCACCCGCG
680 X 690 700

10. US-09-746-783-18 (1-481)

US-09-096-287-9 Sequence 9, Application US/09096287

Initial Score = 59 Optimized Score = 179 Significance = 0.72
Residue Identity = 39% Matches = 194 Mismatches = 287
Gaps = 6 Conservative Substitutions = 0

60 70 80 90 100 110 120
GGATTTTCATCAGCACTCCCTGGTGTATCATGTACAGATTATTAAGACAGATGAATTTAAACATTT
TATCCATATTGATTCACATATTCATTATTAAGCTTTCTGGTACATATTTCTGGGCTCTTGGCGTAG
2260 2270 X 2280 2290 2300 2310 2320

130 140 150 160 170 180 190
TTTGACAGCTGCGGACACAAACTCGCAGTGTTCATATTTCTCGAAAGCGTGGTCCCTCCAAAGGAT
TGGGAGAGGACATTTTGAATCTGAAGAATCATATCTGTATATATACATATGAGTGGGAGATGGG
2400 2410 2420 2430 2440 2450 2460

200 210 220 230 240 250 260
GTTT--CTGTGTTTCATGAGCTGCGTGAACCTTGACATCAAAACAAATACCCACATTTCAAGTTCAG
GGTGGCAGGCGGTGAGGAGGACAAACAGTACATGAGGAAAGGACGATCTCGAGTGGGAG
2470 2480 2490 2500 2510 2520 2530

270 280 290 300 310 320 330
AAAGGACAG--AAGGTAACTCTTCATGAATCAAAAGAAATTAATTTGCTGTATAGAGTGCATCATGA
GTACCTGGGTCGCTGTCTCTCTGTATGCTGTGGTATATGACACTATATACCTTCCCTGTGTA
2540 2550 2560 2570 2580 2590 2600 2610

340 350 360 370 380 390 400
G--CAACCTGATTTTGTGAGCTTGTGAGCCGATGCTTAAATAATTGGNACCAAGACTCAAGATTTATGTA
GTTCAATGCTCTGTGAGCTTGTGAGCTTGTGAGCCCTGATGACACTCAAGGACATTAAGTCAAGAA
2620 2630 2640 2650 2660 2670 2680

410 420 430 440 450 460 470
AGCTGATCTCCAGGCAAAATACATTTGACATTTGAAAGCAAAAAAATTAATTAATTAATTAATTAATTA
CTGAACCTCGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
2690 2700 2710 2720 2730 2740 2750

X
AAA
111
AAAAA
2760 2770

11. US-09-746-783-18 (1-481)

US-09-185-936-9 Sequence 9, Application US/09185936

Initial Score = 58 Optimized Score = 172 Significance = 0.69
Residue Identity = 41% Matches = 211 Mismatches = 260
Gaps = 34 Conservative Substitutions = 0

AAACACTGTGTCAGGCTCTGCGGAGAGTTGACTACATGTAGCTCTTGATTTATATGAATTTGCTTC
780 790 800 810 820 830 840 850

60 70 80 90 100 110 120
GGATTTTCATCAGCACTTC--CTGGTGTATCATGTACAGATTATTAAGACAGCAATGAATTAACAT
AGATTTATTTTCACTCTGCTCTTCCATTTATTTCCAGACAGACACCAAGAGCGCTGTAGAAAAGACT
860 870 880 890 900 910 920

130 140 150 160 170 180
TTTGGACAGCT-----GCCGACACAAACTGCGAGTGTTCATATTTCTTGAAGCGTGGTGC
TTCAGACACCTAGCAATATATATCATATGACACCTGTTTAAAGGGGTCAATCTATGAAACATATGTA
930 940 950 960 970 980 990

190 200 210 220 230 240 250
CTGCAAAAGAGATGTTCCGTTTCCATGAGCTGGCTGAACCTTGCAGATCAAAACATATCCACATTC
AARAGATTGATGACAGACTCAGACATTAAGAAACAAACAAAGAGATGGCTATTCTGCAATTTAG
1000 1010 1020 1030 1040 1050 1060

260 270 280 290 300 310 320
AGATGTTCAAGAAAGCGCAGAGATACCTATTCAGAAATCAAGAAATATTTGCTGTATAGAGTG
TCATG-----ACATTCCTATGATGATGAGATGCTC--ATACAGATTTATGCTTTCCAAATTTGACTT
1070 1080 1090 1100 1110 1120

330 340 350 360 370 380 390
GATTTCAGACCAACCTGATTTTGTGAGTTTGTGAGCGCATGCT--AAAAATTTGAAGCCAGACTCAAGA
GTTTGATTTGCAAAACAAATTTATCTGTTTGAAGCAAGATGTTGAATGATTTATATATGATGAT
1130 1140 1150 1160 1170 1180 1190 1200

400 410 420 430 440 450 460
TTAATGTAACTGATCTTCAAGCAAAATACCTTGTGACATTTGAAAGCCAAATTAATTAATTAATTA
TTAAAGCTTGGTATCTTATATGATGAGCTTACATTTGTAACATTTGTAATTAATTAATTAATTAATG
1210 1220 1230 1240 1250 1260 1270

470 480
-----AAAAA
GTTTAAAAA
1280 1290 X

12. US-09-746-783-18 (1-481)

US-09-149-633-15 Sequence 15, Application US/09149633

Initial Score = 57 Optimized Score = 175 Significance = 0.67
Residue Identity = 39% Matches = 192 Mismatches = 286
Gaps = 12 Conservative Substitutions = 0

ACCTTTCGCTTTAGAGCTTAACCTGAGATTTGTGTGTAAGGTTCCAAAGATCATGTAATTAAGGAGAT
340 350 X 360 370 380 390 400

60 70 80 90 100 110 120
GGATTTTCATCAGCACTTCCCTGTTATCATGTATCAAGATTATTAAGACAGCAATGAATTTAAACAT
TTTCAATTTTCAATTTTCCATGCAAAACATCATTTATTAATTAATTAATTAATTAATTAATTAATTA
410 420 430 440 450 460 470

130 140 150 160 170 180
TTTGAAGCTGCGGACACAAACTCGCAGTGTTCATTT-----TTCTTCAAGAAACGGTGTGCTCG
TACAACTAATTAATGACAGAAATGACGCTTATTAATTTCTAGTATGATCAAAAGATGATGCTG

```
480 490 500 510 520 530 540 550
190 200 210 220 230 240 250
CAAAAGAGTTTCTGTTTCCAGTGCAGTGAACCTGACATCAAAATACCCACATTTCAGAT
-AAAATTACAGTAATATTTATATATCT-TAGAAATCTCAAGACGTGGAATAGGAAGAGAGT
560 570 580 590 600 610 620
GTTCAAGAAAGCCAGAGTACCTATCTATCTCAAGATCAAAAGATTAATTTGCTGTATAGAGTGAT
TCTGGCCCAATCTTAGAGAAATCACCACGTTCGGTATATACCTGCTCTGATCGCTTAGAGATCTT
630 640 650 660 670 680 690
340 350 360 370 380 390 400
CATGACCAACCTGATTTTGTGAGTGGAGCCGATGTAATAATTTGAGCCCAAGCAATCAAGATTAT
-AAAATTACAGTAATATTTATATATCT-TAGAAATCTCAAGACGTGGAATAGGAAGAGAGT
700 710 720 730 740 750 760
410 420 430 440 450 460 470
GTAAGCTGATCTCCAGGCAAAATACCTGTGACATTTGAAAAAGCAAAAAAATTTGAAAAA
GAAAGCTTTATCTAGAGAAAAAATTTAGAAAAATGATATCTGATCTGATCTGAAATGCGGAA
770 780 790 800 810 820 830
480
AAAAA
AAAAATTAATGTTAAAAAACTAT
840 X 850 860

13. US-09-746-783-18 (1-481)
US-09-096-287-17 Sequence 17, Application US/09096287

Initial Score = 55 Optimized Score = 158 Significance = 0.62
Residue Identity = 34% Matches = 170 Mismatches = 311
Gaps = 10 Conservative Substitutions = 0

X
60 70 80 90 100 110 120
GATATCTGTAATTAATAGAGACAGCTACGATCTGATCAACTAAACCAACG
CAGATAGAAACCCAGCTGGGTCCTTATGAGCCGACCTCCCAAGCAAGCTGCTCTCCAGC
800 810 X 820 830 840 850 860
60 70 80 90 100 110 120
GATATCTGTAATTAATAGAGACAGCTACGATCTGATCAACTAAACCAACG
CAGATAGAAACCCAGCTGGGTCCTTATGAGCCGACCTCCCAAGCAAGCTGCTCTCCAGC
870 880 890 900 910 920 930
130 140 150 160 170 180
TTTG--ACAAGCTGGGACACAAAGTGCAGTGTTCATTTTCTG-----AAAGCTGTGCTCCT
TGGCTCTGAGACCTCCCAAGCTGCTTACAGCTCATTTCTGCTGGGAGTAGAGAGGAGAGTAA
940 950 960 970 980 990 1000 1010
190 200 210 220 230 240 250
GCAAAAGAGATTTCTGTTTCCAGTGCAGTGTTCATTTTCTG-----AAAGCTGTGCTCCT
GTTAAACCTTGGACAGTAAGAGCTGGGAGAGCTGCTGCTCCTGCTCCTCAGCACTGAT
1020 1030 1040 1050 1060 1070 1080
260 270 280 290 300 310 320 330
TGTTCAAGAAAGCCAGAGTACCTATTTCAAGATCAAAAGATTAATTTGCTGTATAGAGTGAT
ATAGTGTGAAAGCTGGGAGATTTCTGATGCGGCAATGCTGTTTCTCTCCCTCCACCTCTCAG
1090 1100 1110 1120 1130 1140 1150
340 350 360 370 380 390 400
TCATGAGCAACCTGATTTTGTGATTTTGTGAGCCGATTAATAATTTGGAAGCCACAGCTCAAGATTAA
-AAAATTACAGTAATATTTATATATCT-TAGAAATCTCAAGACGTGGAATAGGAAGAGAGT
1160 1170 1180 1190 1200 1210 1220
GAGCAGAGAGCGGACGACGACCTGTAGAGCAGATGCTTTGCCCTCCCTCCCTGGAAGTC
1160 1170 1180 1190 1200 1210 1220
410 420 430 440 450 460 470
TGTAACCTGATCTCCAGAGCAAAATACCTTTGTGACATTTGAAAGCAAAAAAATTTGAAAA
TTGGGCTCTGAGTGTGCAAGACGCGCTGTGGCAAAATAAAGAGCTGTTGTTTACTTAAAAAA
1230 1240 1250 1260 1270 1280 1290
480
AAAAA
AAAAATTAATGTTAAAAAACTAT
1300 X

14. US-09-746-783-18 (1-481)
US-08-958-304-17 Sequence 17, Application US/08958304

Initial Score = 54 Optimized Score = 173 Significance = 0.60
Residue Identity = 38% Matches = 190 Mismatches = 291
Gaps = 11 Conservative Substitutions = 0

X
60 70 80 90 100 110
GATATTTT-----CATGACCTTCCCTGCTGATATCATGATGATTAATAAGACAGAAATTT
AGGTTTTCCTCCGCTTTGAAACATTTGCTTATGAGAGTGTTCATATTTTATCTGAGTAGACA
490 500 510 520 530 540 550 560
120 130 140 150 160 170 180
GAAAGCTTTTATCTAGAGAAAAAATTTAGAAAAATGATATCTGATCTGATCTGAAATGCGG
TAAATATCAATTTTATCTAGATGCAAGAGTACATTTGGCAAAAGTTCAGCATTAATTAAC
570 580 590 600 610 620 630
190 200 210 220 230 240 250
GCAAAAGATTTTCTGTTTCCAGTGCAGTGTTCATTTTCTGCA--AAAGCTGTGCTCCT
CTGTTAGCAATATTTCTTGAATAAAAGTCCAGTCTTATGATTAAGCAAGCCCATTAATTA
640 650 660 670 680 690 700
260 270 280 290 300 310 320
TGTTCAAGAAAGCCAGAGTACCTATTTCAAGAA--TCAAAAGATTAATTTGCTGTATAGAGTGA
MTGTGNGGACTGAAACNGTACCTTATATTTATGCTAAAGGAAATGAGATTAACTTCTCCTACAGGCCAN
710 720 730 740 750 760 770
330 340 350 360 370 380 390 400
TTTCATGCAACCTGATTTTGTGAGTGGAGCCGATGCTAAATAATTTGAGCCAGCACTCAAGATTA
AACCANAAAGGCTTCAGCAACCTGATTAATAANTANTTTGCGCATNTCAAGCAATTTGTTGATAT
780 790 800 810 820 830 840
410 420 430 440 450 460 470
ATGTAAGCTGATCTCCAGAGCAAAATACCTTTGTGACATTTGAAAGCAAAAAAATTTGAAAA
TTATGATCTTTTCTTATCTGATGAAATTTGCAATTAAGCATGAGATCTTAATTAATTAATTA
850 860 870 880 890 900 910 920
AAAAA
AAAAATTAATGTTAAAAAACTAT
AAAGCGCGCAGAGTCTAGATTCATC
930 940

15. US-09-746-783-18 (1-481)
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270
AAGAAACCCGAGAGTACCCTTTCTCAAGAATCATAAAGATANTATTTCCTTTTACAAGTGATTCATCATC
280
| | | | | | | | | | | | | | | | | | | | | |
290
TTTATGACACGTATAGAAACTTCATCTTGAAGCAACTTCCTTAACATGATGGGTTTTTATTATTTCATTCGCAT
300
| | | | | | | | | | | | | | | | | | | | | |
310
| | | | | | | | | | | | | | | | | | | | | |
320
| | | | | | | | | | | | | | | | | | | | | |
330


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CAGACATAAGTATGATGAGCCCTCTGTATTCGCTGACAGCCCTGCTTAAAGCTTTATATAGCT
1650      1660      1670      1680      1690      1700      1710      1720
      130      140      150      160      170      180      190
TTTGACAGCTGCCGACACAAACGCGAGTGTCTCATTTTCTCGAAACGGTGTGCTCCCTGCAGAAAGAT
      1      1      1      1      1      1      1
GACTGAATATCTGTATGCAATTTTAAAGTATTTAACTAACACTAGGATTTGCTAACTAGCTTTCAATCAAAA
1730      1740      1750      1760      1770      1780      1790
      200      210      220      230      240      250      260
GTTTCCGTGTTTCCATGAGCTGGCTGAACCTTGTCACATCAAAACAAATACCCACATTTGAGATGTTCAAGAA
      1      1      1      1      1      1      1
ATGGGACCATGGCTATTAAGACAACTATATATTTTATATATGTTTCTGAAGTAACATT--GTAATCATAGATT
1800      1810      1820      1830      1840      1850      1860
      270      280      290      300      310      320      330
AAGCCAGAAAGGTACCCCTATTTCTCAAGAAATCAAAAGAAATATTTGCTGTATAGAAAGTGATTCATGACCAA
      1      1      1      1      1      1      1
AACATTTTAAATTAACATTAATCAATGCTATGTAAATATAAGACTACTGCTTTGTGAGGGAATGTTTGTGCAA
1870      1880      1890      1900      1910      1920      1930
      350      360      370      380      390      400      410
CCTGATTT--TTGAGTTTGTGGAGCCGATGCTAAAAAATGGAAAGCCAGACTCAAGAAATTAATGTAGCT
      1      1      1      1      1      1      1
AATTTTTCCTTAATGATTAATAGTGTAAATGATTAAAAATCTTCAGAAATTAATATTTCCCTTTGTCA
1940      1950      1960      1970      1980      1990      2000
      420      430      440      450      460      470      480
GATCTCAAGGCAAAATACACTGTGTGACATTTGAAAGGCAAAAAAATTTTAAAAAATTTTAAAAAATTTT
      1      1      1      1      1      1      1
CTTTTGAATAACATTAATTAATCAATTTGTATCTGTGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTT
2010      2020      2030      2040      2050      2060      2070
      2080      2090      2100
AAAAAAAAAAAAAAAAAAAAA
X
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